

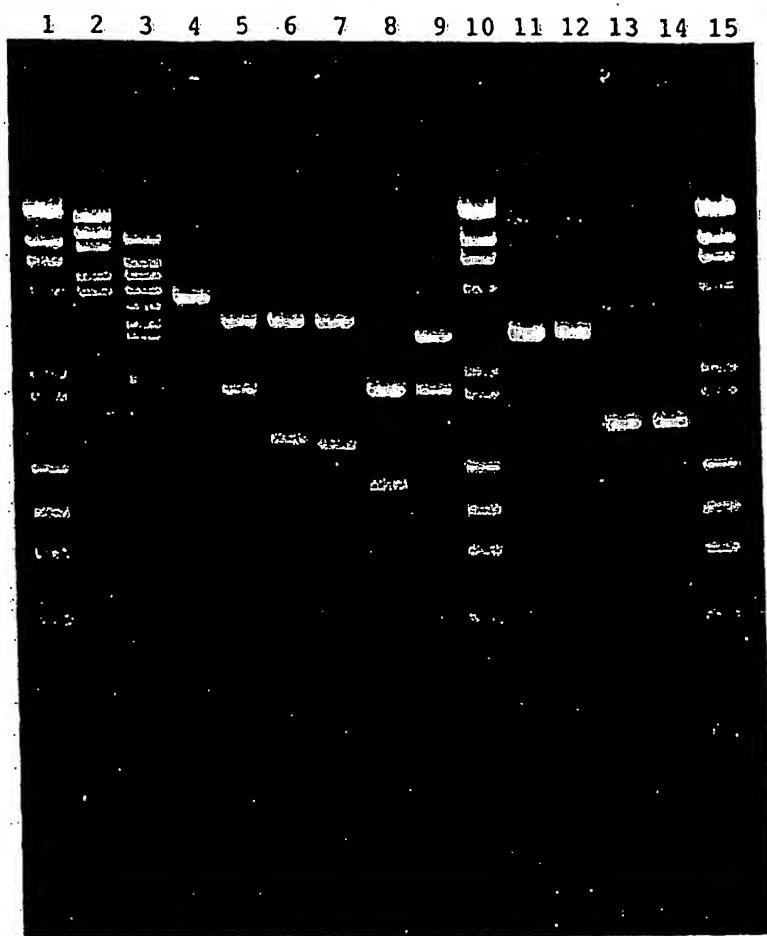
**Figure 1**

Figure 2

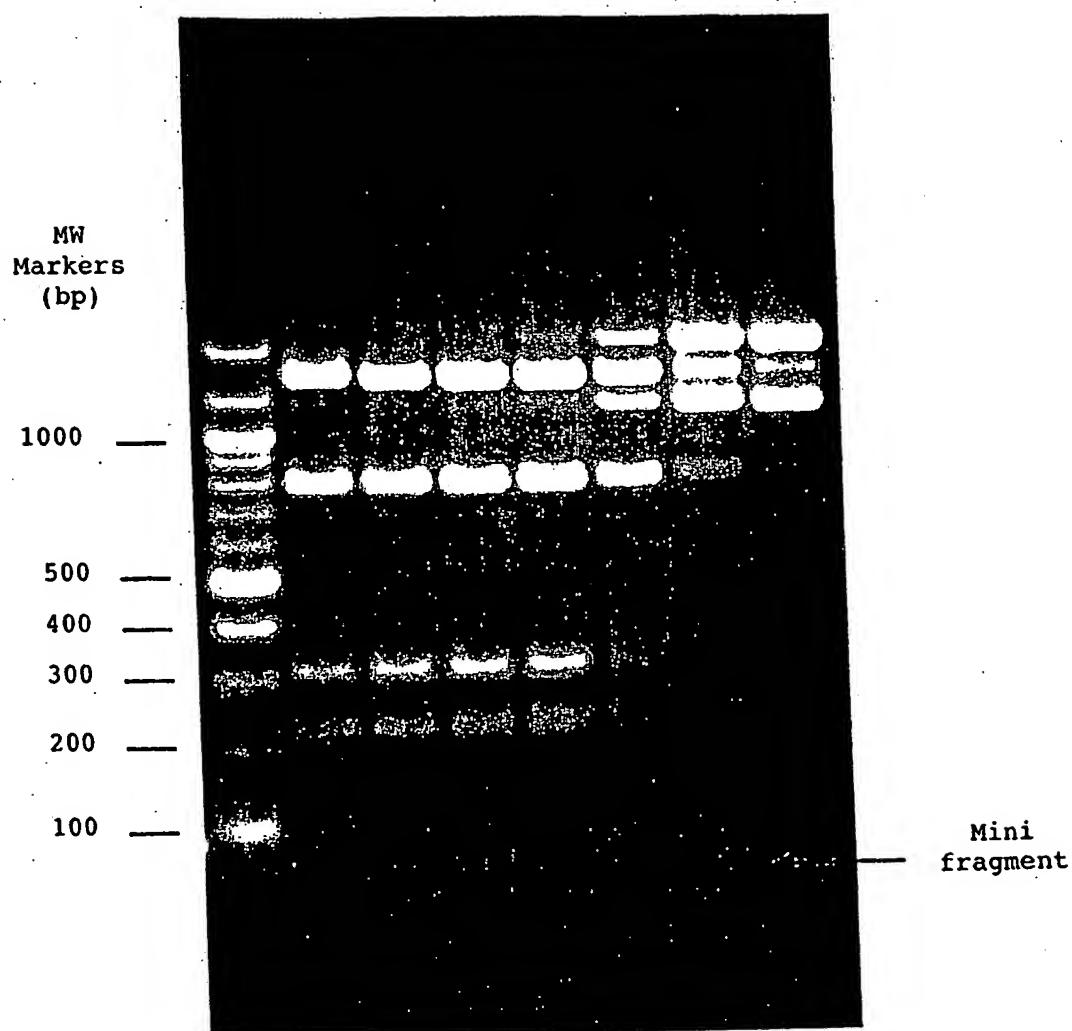


Figure 3

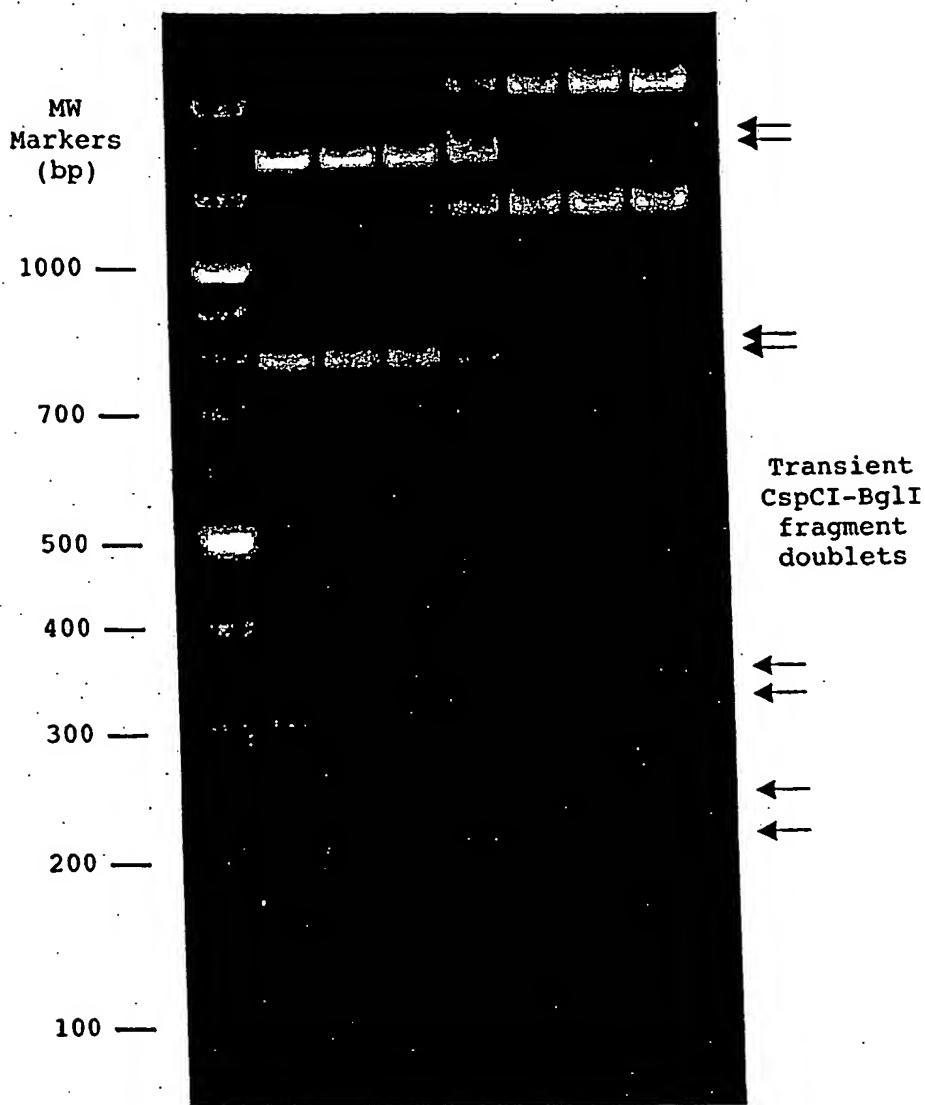


Figure 4a

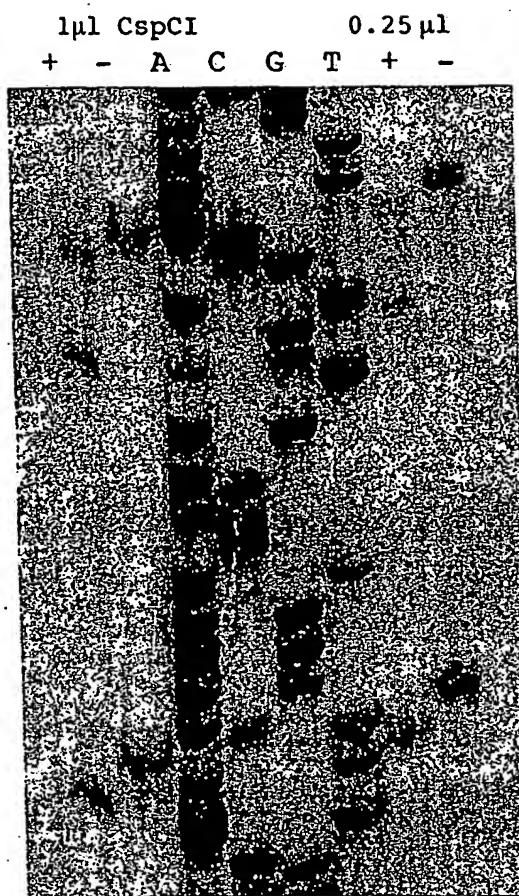
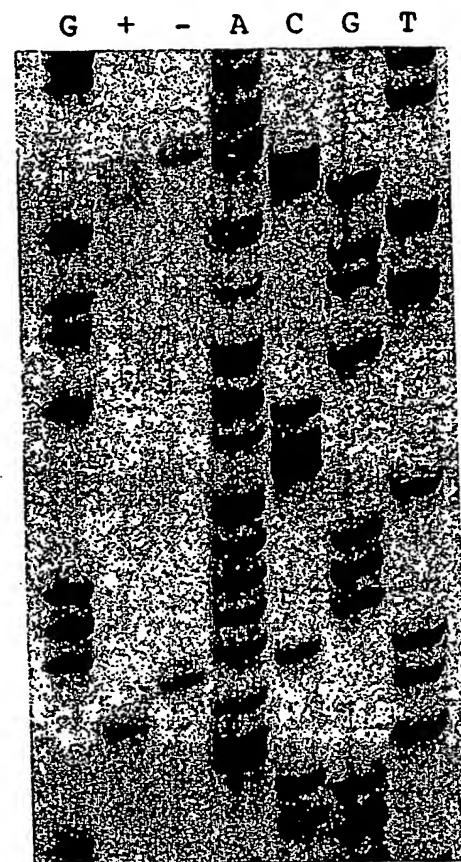


Figure 4b



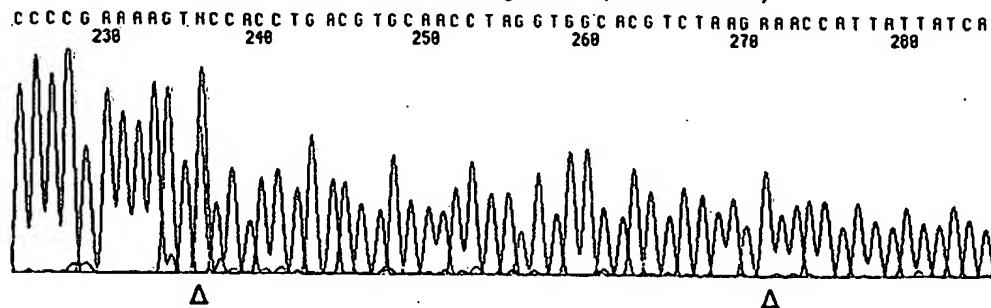
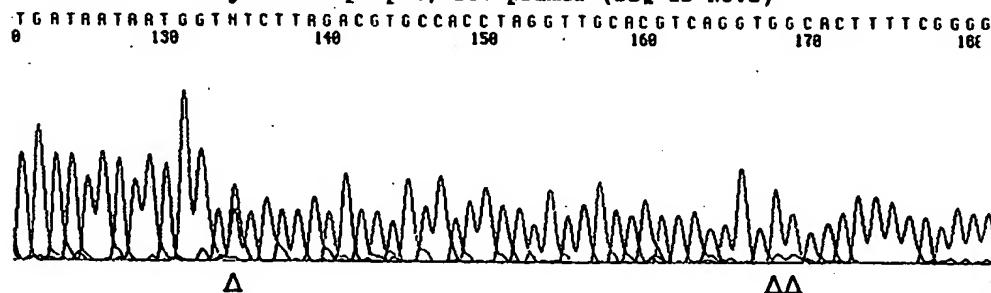
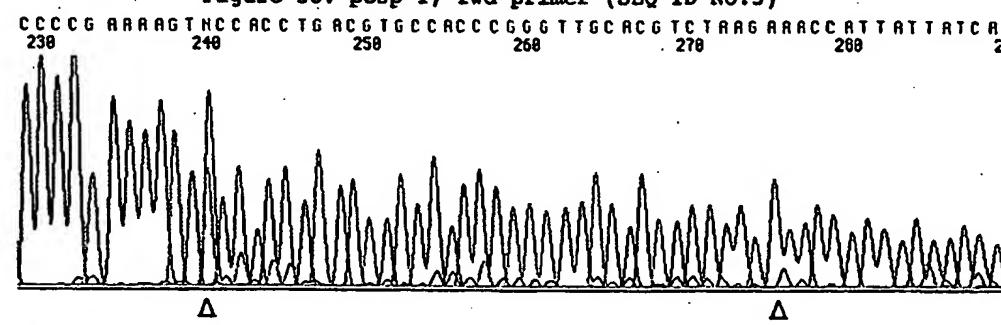
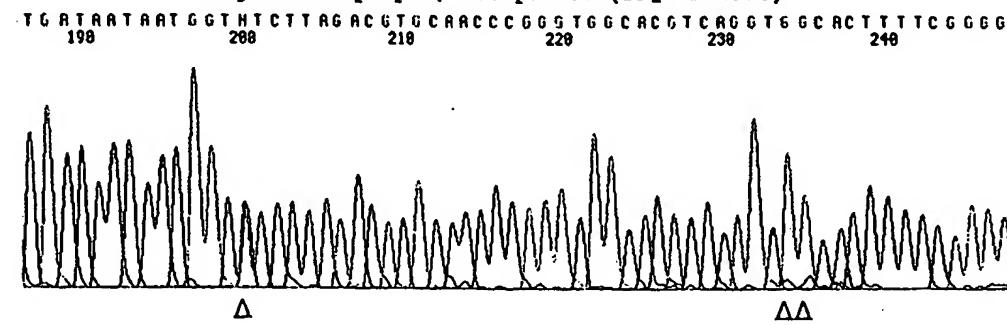
**Figure 5a. pCsp-4, fwd primer (SEQ ID NO:1)****Figure 5b. pCsp-4, rev primer (SEQ ID NO:2)****Figure 5c. pCsp-1, fwd primer (SEQ ID NO:3)****Figure 5d. pCsp-1, rev primer (SEQ ID NO:4)**

Figure 6-2

2151 TGCACGAGTT TATTTGGACG AAGGCAAAAA TCTCCGAAGA AGAAAAGCCT  
 2201 CTGCTGGTGA GTGGGACCTT GATTGCGTTG ATGAACAACA CATTCACTAA  
 2251 GACCTTGTAC GCTCTACCTG CAGAAGATGT GCAGGAAGCG TGGCTGACGG  
 2301 CTATCAAGAA GGAGCTGGAC AAAGCTTCTA TCCCCCAGGC CAAGAAGGAC  
 2351 ACGATGCTGC AGCCGTATAC GACGATTGCG GTTAATCCCA ATCTTGCGAA  
 2401 GCCTGACAGC AAGACGGCTA AAGAGTATCC AGATGGAGTT TTCAGGGAAA  
 2451 TAATCACCCG CATCGCCGAC AACGTCTGGC CCTACATCAA TGTCTTCAC  
 2501 GACTTGATG TGGTCGGACA ATTCTACGGT GAGTTCTGA AATATACTGC  
 2551 GGGCGACAAA AAAGCGCTGG GCATCGTGC GACGCCGCGC CATGTGGCTG  
 2601 AACGTGTTCTC GCTCATCGCC AACGTTAAC CCAAGTCTAA GGTGCTGGAC  
 2651 ATCTGTGCGG GCACGGCGG CTTCTCATC TCAGGCCATGC AACACATGCT  
 2701 CAAGAAGGCC GTAACGGACA AAGAGCGCAA CGACATCAAG CAAAATCGGC  
 2751 TCATCGGGAT TGAAAACAAC CCCAAGATGT TTGCCCTGGC TGCCAGCAAC  
 2801 ATGATTCTGC GTGGTGATGG TAAGGCTAAC CTGCACCAGG CCAGTTGCTT  
 2851 TGATAATGCA GTGATTGCGG CCGTGCAGAA GATGAAGCCC AACGTGGGCA  
 2901 TGCTTAACCC CCCGTATTG CAGTCCAAGA GCGACGCCGA ACTGCATGAG  
 2951 CTGTATTTCG TCAAGCAAAT GCTCGACACG CTTACACCAAG GTGGAGTTGG  
 3001 TATCGCGATT GTTCCCATGT CAAGGCCAT CTCGCCAAC CCAATGCCGTG  
 3051 AAGAGCTGAT GAAGTACAC TCACTGGATG CGGTCATGTC AATGCCCAAG  
 3101 GAGCTGTTT ATCCAGTGGG CACGGTCACC TGTGTATGG TCTGGATTGC  
 3151 CGGTGTGCCA CATGAGCAAA TGTCCAAGAA GACATGGTTT GGCTACTGGC  
 3201 GCGACGATGG CTTTGTGAAA ACCAACGATA AGGGGCCAT CGACATGAAT  
 3251 GGCACCTGGC CAGACATCCG TGACCGATGG ATTGAAATGT ATCGCAATCG  
 3301 CGAAGTGCAT GCTGGCGAGA GCATCATGCA GAAGGTAGGC CCCGATGATG  
 3351 AATGGTGCAG TGAAGCCTAT ATGGAAACGG ACTACTCAGT GCTGACTCAG  
 3401 TCCGACTTTG AGAAGGTCGT TCAAAGCTAC GCGCTATTTA AACTATTGG  
 3451 TCAAGGCAGT AGCCAGTCCG AAGTGAAAGG GGCAACGGAT GCCGAAGATT  
 3501 AACGACCTT TTCATCTGGA GTACGGTCAC AGCCCTGGAGT TGAACCGGCT  
 3551 AGAGCAATCC ACAGCAGCCG ATGCCGTCAA CTTCGTTGGA CGGGCAGCTA  
 3601 GGAACAATGG AGTCACCGCA CGCGTGGCTC CCCCTCCAAA CTTGAAACCG  
 3651 GCAGCCGCAG GCACCATCAG CGTAGCGCTG GGAGGGCAAG GTGGCGCAGG  
 3701 AGTCGCCTTC CTCCAACCGC GTCCCTACTT TTGTGGCCGC GATGTGATGG  
 3751 TGCTGACCCCA CAAGAACGAC ATGACAGACC AAGAAAAGCT GTGGTGGGTC  
 3801 ATGTGCATCA CAGCCAACCG TTTCCGTTT GGATTTGGTC GCCAAGCTAA  
 3851 TCGGACGCTA AAGGACTTGA ATCTGCCTGC GCCCCAAAAA ACTCCAAGCT  
 3901 GGGTGCATAC AGCGAACCCC GATGCCCTACC AAGGTGTCAG GTCCCCCGCA  
 3951 AGTGTTCATC CAGTCGGCAC GCTGGCTGTG AGCAACTGGA AGGTTTCAT  
 4001 TCTTCAAGAC TTGTTTACCA TCCGTAAAGG ACAGCGACTC ACCAAGGCCA  
 4051 ACATGTTGCC CGGTACGGTG CCCTACATCG GCGCATCGGA CACTTCCAAC  
 4101 GGC GTTACTG CGCACATCGG GCAAAAACCA ATCCACGAGG GCGGCACCAT  
 4151 CAGCGTCACA TATGACGGTT CAATAGCTGA AGCGTTTAC CAGCCCTCCC  
 4201 CATTGGGC ATCGGATGCT GTGAACGTGC TCTATCCCA GGGTTTCACA  
 4251 CTCACACCGG CCACTGCCTT GTTTATCTGC GCAATCATCA GGATGGAGAA  
 4301 ATATCGCTTC AACTATGGCC GAAAATGGCA CTTAGAGCGT ATGCGAGAGA  
 4351 CAGTTATCAG GTTACCGACT ACTGCAACAG GTGCACCCAGA TTGGGACTTT  
 4401 ATGGAGAAAT ACATCAAAAC TTTGCCCTAT AGCTCGCAGT TGCAATAATC

**Figure 6-3**

4451 ATGGCTGATT TCCTAAATTT CCTGCCGCAT CTACGGGTAT TGCATGTTCA  
4501 GGACGGTGGT GATCATCGCT AGGTGGAGGC GGAAAGCCGT GTTTTGCTGA  
4551 CCGCTTGCCTT GGCCTGCGGT GAAAAGCCTT CCCATTCAGG GAAGGCTTTA  
4601 ATCGAGTTAT AGATCT

Figure 7a (SEQ ID NO:6)

1 ATGGCGAACG AACGCAAAAC AGAATCCTTA GTTCGAGACC AGCTACGGAC  
 51 ATTGGCTAC TACGAACCCG ACAACGGCAT TTCTGTAGAG GAGCAAAAGT  
 101 CCGAGATTGT CAAGATTAAG GGTTTGCTTT CAAAAGCAAG TAAGAACGCC  
 151 AAGGGCAATA TTGGTTATCC CGAGTTCATC ATCTCTAACCC GGAAAGATAC  
 201 TGCATTCCCTG ATAGTTGTGG AGTCAAGGCC GGATGTGAAA AAGCACGAGA  
 251 GCCCAAGCCG TGATAAGCCG GTAGACTATG CGGTGGATGG CGTTCTCAC  
 301 TACGCCAGAC ACCTAGCCAA GCACATACCC GTATTGGCGG TGGCTGTGAG  
 351 CGGCACGACG GCAAGTTCTA TCAAGGTGTC CAACTCCCTT GTGCCTGCGG  
 401 GTACCAACGGA TGTGAAGGCG CTGGTCAACG AGAGTAATTC CTCAGTTGCC  
 451 GAATTGGTGC CTTATGATGA CTACTACCGC CTGGCGTCTT ATGATCCGA  
 501 TGTGCTCAG AAGCGCCACT CTGACTTGCT GGCCTCTCA CGCGAGCTGC  
 551 ACGAGTTTAT TTGGACGAAG GCAAAAATCT CCGAAGAAAGA AAAGCCTCTG  
 601 CTGGTGAGTG GGACCTTGAT TGCGTTGATG AACAAACACAT TCATCAAGAC  
 651 CTTGACGCT CTACCTGCAG AAGATGTGCA GGAAGCGTGG CTGACGGCTA  
 701 TCAAGAAGGA GCTGGACAAA GCTTCTATCC CCCAGGCCAA GAAGGACACG  
 751 ATGCTGCAGC CGTATACGAC GATTGCGGTT AATCCAATC TTGGCAAGCC  
 801 TGACAGCAAG ACGGCTAAAG AGTATCCAGA TGGAGTTTC AAGGAAATAA  
 851 TCACCCGCAT CGCCGACAAC GTCTGGCCCT ACATCAATGT CTTTCACGAC  
 901 TTTGATGTGG TCGGACAATT CTACGGTGAG TTTCTGAAAT ATACTGCGGG  
 951 CGACAAAAAA GCGCTGGGCA TCGTGCTGAC GCCGCGCCAT GTGGCTGAAC  
 1001 TGGTCTCGCT CATGCCAAC GTTAACCCCA AGTCTAAGGT GCTGGACATC  
 1051 TGTGCGGGCA CGGGCGGCTT TCTCATCTCG GCCATGCAAC ACATGCTCAA  
 1101 GAAGGCCGTA ACGGACAAAG AGCGCAACGA CATCAAGCAA AATCGGCTCA  
 1151 TCGGGATTGA AAACAACCCC AAGATGTTG CCTTGGCTGC CAGCAACATG  
 1201 ATTCTGCGTG GTGATGGTAA GGCTAACCTG CACCAGGCCA GTTGCTTGA  
 1251 TAATGCAGTG ATTGCGGCCG TGCAGAAGAT GAAGCCCAAC GTGGGCATGC  
 1301 TTAACCCCCC GTATTCGCAG TCCAAGAGCG ACGCGGAAC GCATGAGCTG  
 1351 TATTCGTCA AGCAAATGCT CGACACGCTT ACACCAGGTG GAGTTGGTAT  
 1401 CGCGATTGTT CCCATGTCAA GGCACATCTC GCCCAACCCCA ATGCGTGAAG  
 1451 AGCTGATGAA GTACCACTCA CTGGATGCGG TCATGTCAAT GCCCCAGGAG  
 1501 CTGTTTATC CAGTGGGCAC GGTACACCTGT GTCAATGGTCT GGATTGCCGG  
 1551 TGTGCCACAT GAGCAAATGT CCAAGAAGAC ATGGTTGGC TACTGGCGCG  
 1601 ACGATGGCTT TGTAAAACC AAGCATAAAGG GGCGCATCGA CATGAATGGC  
 1651 ACCTGGCCAG ACATCCGTGA CCGATGGATT GAAATGTATC GCAATCGCGA  
 1701 AGTGCATGCT GGCAGAGAGCA TCATGCAGAA GGTAGGCCCG GATGATGAAT  
 1751 GGTGCGCTGA AGCCTATATG GAAACGGACT ACTCAGTGT GACTCAGTCC  
 1801 GACTTTGAGA AGGTCGTTCA AAGCTACCCG CTATTAAAC TATTTGGTCA  
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Figure 7b (SEQ ID NO:6)

1 ATGCCGAAGA TTAACGACCT TTTTCATCTG GAGTACGGTC ACAGCCTGGA  
51 GTTGAACCGG CTAGAGCAAT CCACAGCAGC CGATGCCGTC AACTTCGTTG  
101 GACGGGCAGC TAGGAACAAT GGAGTCACCG CACCGCGTGGC TCCCCCTCCA  
151 AACATTGAAAC CGGCAGCCGC AGGCACCATC AGCGTAGCGC TGGGAGGGCA  
201 AGGTGGCGCA GGAGTCGCCT TCCTCCAACC GCGTCCCTAC TTTTGTGGCC  
251 GCGATGTGAT GGTGCTGACC CCCAAGAAGC ACATGACAGA CCAAGAAAAG  
301 CTGTGGTGGG TCATGTGCAT CACAGCCAAC CGTTCCGCT TTGGATTGG  
351 TCGCCAAGCT AATCGGACGC TAAAGGACTT GAATCTGCCT GCGCCCCAAA  
401 AAACTCCAAG CTGGGTGCAT ACAGCGAACCC CGATGCCTA CCAAGGTGTC  
451 AGGTCCCCCG CAAGTGTCA TCCAGTCGGC ACGCTGGCTG TGAGCAACTG  
501 GAAGGCTTTC ATTCTTCAG ACTTGTTAC CATCCGTAAA GGACAGCGAC  
551 TCACCAAGGC CAACATGTTG CCCGGTACGG TGCCCTACAT CGGCGCATCG  
601 GACACTTCCA ACGGCGTTAC TGCGCACATC GGGCAAAAAC CAATCCACGA  
651 GGGCGGCACC ATCAGCGTCA CATATGACGG TTCAATAGCT GAAGCGTTTT  
701 ACCAGCCCTC CCCATTGG GCATCGGATG CTGTGAACGT GCTCTATCCC  
751 AAGGGTTTCA CACTCACACC GGCCACTGCC TTGTTTATCT GCGCAATCAT  
801 CAGGATGGAG AAATATCGCT TCAACTATGG CCGAAAATGG CACTTAGAGC  
851 GTATGCGAGA GACAGTTATC AGGTTACCAAG CTACTGCAAC AGGTGCACCA  
901 GATTGGGACT TTATGGAGAA ATACATCAAAC ACTTTGCCCT ATAGCTCGCA  
951 GTTGAATAA

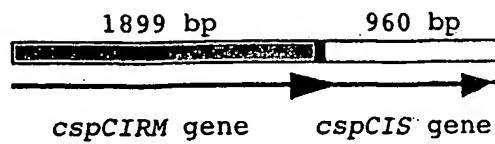


Figure 8a

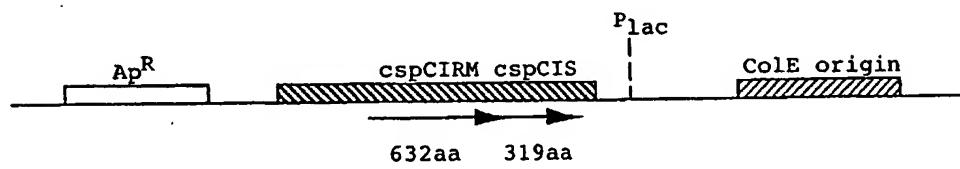


Figure 8b

Figure 9a (SEQ ID NO:8)

1 MANERKTESL VRDQLRTFGY YEPDNGISVE EQKSEIVKIK GLLSKASKNA  
51 KGNIGYPEFI ISNRKDRAFTL IVVECKPDVK KHESPSRDKP VDYAVDGVLH  
101 YARHLAKHYT VLAVAVSGTT ASSMKVSNFL VPAGTTDVKA LVNESNSSVA  
151 ELVPYDDYYR LASYDPDVAQ KRHS DLLAFS RELHEFIWTK AKISEEEKPL  
201 LVSGTLIALM NNTFIKTFDA LPAEDVQEAW LTAIKKELDK ASIPQAKKDT  
251 MLQPYTTIAV NPNLGKPDSK TAKEYPDGVF KEIITRIADN VWPYINVHD  
301 FDVVGQFYGE FLKYTAGDKK ALGIVLTPRH VAELFSLIAN VNPKSKVLDI  
351 CAGTGGFLIS AMQHMLKKAV TDKERNDIKQ NRLIGIENNP KMFALAASN  
401 ILRGDGKANL HQASCFDNAV IAAVQKMKPN VGMLNPPYSQ SKSDAELHEL  
451 YFVKQMLDTL TPAGVGIAIV PMSSAISPNNP MREELMKYHS LDAVMSMPQE  
501 LFYPVGTVC VMVWIAGVPH EQMSKKTWFG YWRDDGFVKT KHKGRIDMNG  
551 TWPDIDRDRWI EMYRNREVHA GESIMQKVGP DDEWCAEAYM ETDYSVLTQS  
601 DFEKVVQSYA LFKLFGQGSS QSEVKGATDA ED

Figure 9b (SEQ ID NO:9)

1 MPKINDLFHL EYGHSLLELR LEQSTAADAV NFVGRAARNN GVTARVAPPP  
51 NLKPAAAGTI SVALGGQGGA GVAFLQPRPY FCGRDVMVLT PKKHMTDQE  
101 LWWWMCITAN RFRFGFGRQA NRTLKDNLNP APQKTPSWVH TANPDAYQGV  
151 RSPASVHPVG TLAVSNWKAF ILQDLFTIRK QRQLTKANML PGTVPYIGAS  
201 DTSNGVTAHI GQKPIHEGGT ISVTYDGSIA EAFYQPSPFW ASDAVNVLYP  
251 KGFTLTPATA LFICAIIRME KYRFNYGRKW HLERMRETVI RLPATATGAP  
301 DWDFMEKYIK TLPYSSSQLQ